0590
1/26

#12

OIPE

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RAW SEQUENCE LISTING   DATE: 12/10/2002 P.6
PATENT APPLICATION: **US/10/037,311A** TIME: 15:43:38

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Output Set: **N:\CRF4\12102002\J037311A.raw**

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 5 <120> TITLE OF INVENTION: XYLOGLUCAN FUCOSYLTRANSFERASES
 7 <130> FILE REFERENCE: MS00-001C2
 9 <140> CURRENT APPLICATION NUMBER: US 10/037,311A
10 <141> CURRENT FILING DATE: 2001-11-09
12 <150> PRIOR APPLICATION NUMBER: US60/117,555
13 <151> PRIOR FILING DATE: 1999-01-28
15 <160> NUMBER OF SEQ ID NOS: 15
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35           35                  40                  45
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39       50                  55                  60
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43 65                  70                  75                  80
46 Leu Asp Ala Gly Val Phe Pro Asn Val Thr Asn Ile Asn Ser Asp Lys
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55           115                 120                 125
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63 145                 150                 155                 160
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67               165                 170                 175
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74 Phe Leu Tyr Ala Leu Leu Thr Asp Arg Val Leu Leu Val Asp Arg Gly
75           195                 200                 205
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87           .         245                 250                 255
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91           260                 265                 270
94  Tyr Gly Asp His Asp Lys Met Phe Phe Cys Glu Gly Asp Gln Thr Phe
95           275                 280                 285
98  Ile Gly Lys Val Pro Trp Leu Ile Val Lys Thr Asp Asn Tyr Phe Val
99      290                 295                 300
102 Pro Ser Leu Trp Leu Ile Pro Gly Phe Asp Asp Glu Leu Asn Lys Leu
103 305                 310                 315                 320
106 Phe Pro Gln Lys Ala Thr Val Phe His His Leu Gly Arg Tyr Leu Phe
107               325                 330                 335
110 His Pro Thr Asn Gln Val Trp Gly Leu Val Thr Arg Tyr Tyr Glu Ala
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114 Tyr Leu Ser His Ala Asp Glu Lys Ile Gly Ile Gln Val Arg Val Phe
115           355                 360                 365
118 Asp Glu Asp Pro Gly Pro Phe Gln His Val Met Asp Gln Ile Ser Ser
119      370                 375         .         380
122 Cys Thr Gln Lys Glu Lys Leu Leu Pro Glu Val Asp Thr Leu Val Glu
123 385                 390                 395                 400
126 Arg Ser Arg His Val Asn Thr Pro Lys His Lys Ala Val Leu Val Thr
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130 Ser Leu Asn Ala Gly Tyr Ala Glu Asn Leu Lys Ser Met Tyr Trp Glu
131           420                 425                 430
134 Tyr Pro Thr Ser Thr Gly Glu Ile Ile Gly Val His Gln Pro Ser Gln
135           435                 440                 445
138 Glu Gly Tyr Gln Gln Thr Glu Lys Lys Met His Asn Gly Lys Ala Leu
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142 Ala Glu Met Tyr Leu Leu Ser Leu Thr Asp Asn Leu Val Thr Ser Ala
143 465                 470                 475                 480
146 Trp Ser Thr Phe Gly Tyr Val Ala Gln Gly Leu Gly Gly Leu Lys Pro
147               485                 490                 495
150 Trp Ile Leu Tyr Arg Pro Glu Asn Arg Thr Thr Pro Asp Pro Ser Cys
151           500                 505                 510
154 Gly Arg Ala Met Ser Met Glu Pro Cys Phe His Ser Pro Pro Phe Tyr
155           515                 520                 525
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176 ctcacgagaa ccttcactac ttgcttgata gtcttctctg tactagtagc attctcaatg   180
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178 atctttcacc aacacccatc tgattcaaat cggattatgg gtttcgccga agctagagtt  240
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182 tttgatgaag attcttgcct tagtaggtac caatcagttc attaccgtaa accttcacct  360
184 tacaagccat cttcttatct catctctaag cttagaaact acgaaaagct tcacaagcga  420
186 tgtggtccgg gtactgaatc ttacaagaaa gctctaaaac aacttgatca agaacatatt  480
188 gatggtgatg gtgaatgcaa atatgttgtg tggatttctt ttagcggctt agggaacagg  540
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192 gaccgaggga aagacatgga tgatctcttt tgcgagccgt ttctcggtat gtcgtggttg  660
194 ctacctttag atttccctat gactgatcag tttgatggat aaatcaaga atcatctcgt  720
196 tgttatggat atatggtgaa gaatcaggtg attgatactg agggaacttt gtctcatctt  780
198 tatcttcatc ttgttcatga ttatggagat catgataaga tgttcttctg tgaaggagac  840
200 caaacattca tcgggaaagt cccttggttg attgttaaaa cagacaatta ctttgttcca  900
202 tctctgtggt taataccggg tttcgatgat gaactaaaca agctattccc acagaaagcg  960
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208 agagttttcg atgaagaccc gggtccattt cagcatgtga tggatcagat ttcatcttgt 1140
210 actcaaaaag agaaacttct acctgaagta gacacactag tggagagatc tcgccatgtt 1200
212 aataccccca aacacaaagc cgtgcttgtc acatctttga acgcgggtta cgcggagaac 1260
214 ttaaagagta tgtattggga atatccgaca tcaactggag aaatcatcgg tgttcatcag 1320
216 ccgagccaag aaggttatca gcagaccgaa aaaaagatgc ataatggcaa agctcttgcg 1380
218 gaaatgtatc ttttgagttt gacagataat cttgtgacaa gtgcttggtc tacatttgga 1440
220 tatgtagctc aaggtcttgg aggtttaaag ccttggatac tctatagacc cgaaaaccgt 1500
222 acaactcccg atccttcgtg tggtcgggct atgtcgatgg agccttgttt ccactcgcct 1560
224 ccattctatg attgtaaagc gaaaacgggt attgacacgg gaacactagt tcctcatgtg 1620
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239 ctcacgagaa ccttcactac ttgcttgata gtcttctctg tactagtagc attctcaatg  180
241 atctttcacc aacacccatc tgattcaaat cggattatgg gtttcgccga agctagagtt  240
243 ctcgacgccg gagttttccc aaatgttact aacatcagta tgtgttcttc caagtcaaag  300
245 ttttgagctt tattacttta gatctcgttc tttacactac gcatttgcct ctgtatgtcc  360
247 atagctcttg gtcgatttca atttgagatc tatactcata aaaattgagt ctttgtcagt  420
249 cacaagacta ctatttttgg tttgatgttg ttttggtgaa aaagtgctct tttgtttttg  480
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259 ggtactgaat cttacaagaa agctctaaaa caacttgatc aagaacatat tgatggtgat  780
261 ggtgaatgca aatatgttgt gtggatttct tttagcggct tagggaacag gatactttct  840
263 ctagcctcgg ttttttcttta cgcgctttta acggatagag tcttgcttgt tgaccgaggg  900
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267 gatttcccta tgactgatca gtttgatgga ttaaatcaag aatcatctcg ttgttatgga 1020
269 tatatggtga agaatcaggt gattgatact gagggaactt gtctcatct ttatcttcat 1080
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277 catcacttag gtaggtatct ttttcaccca actaaccaag tatggggctt agtcactaga  1320
279 tactacgaag cttacttatc gcatgcggat gagaagattg ggattcaagt aagagttttc  1380
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312 atggaaccaa atgtgacatc ctcatcagat gattcatcac tagtgcagag agatcaagaa   180
314 caaaaaggta aacttacttt cttctttttg ttttgaaatg tttctaaatt tttctttgaa   240
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324 gatggaatca caaggatgca agtatgttgt ttggatgtcg tttagcggat taggaaacag   540
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328 tgaaggaggg gaacagttcg cggatttatt ctgcgaaccg ttcctcgata ccacttggtt   660
330 actaccgaaa gatttcacct tagctagtca gttcagtggc tttggtcaaa actcagctca   720
332 ctgccatgga gatatgctga agaggaaact gattaatgaa tcctctgttt cgtctctgtc   780
334 tcatctctat cttcatctag ctcatgacta caatgagcac gacaaaatgt tcttctgtga   840
336 agaagatcaa aatctcttaa agaatgttcc ttggttgatc atgaggacaa acaacttctt   900
338 tgcaccgtct cttttcttga tttcttcttt cgaagaagag ctcggtatga tgtttcccga   960
340 gaaaggaacg gtttttcacc atttaggtcg ttacctttc catccttcaa atcaagtctg  1020
342 gggactaatc acaagatact atcaagctta cttagccaaa gctgatgaaa ggattggtct  1080
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383         35                  40                  45
386 Ser Asp Asp Ser Ser Leu Val Gln Arg Asp Gln Glu Gln Lys Asp Ser
387     50                  55                  60
390 Val Asp Met Ser Leu Leu Gly Gly Leu Leu Val Ser Gly Phe Lys Lys
391 65                  70                  75                  80
394 Glu Ser Cys Leu Ser Arg Tyr Gln Ser Tyr Leu Tyr Arg Lys Ala Ser
395             85                  90                  95
398 Pro Tyr Lys Pro Ser Leu Leu Leu Ser Lys Leu Arg Ala Tyr Glu Glu
399             100                 105                 110
402 Leu His Lys Arg Cys Gly Pro Gly Thr Arg Gln Tyr Thr Asn Ala Glu
403             115                 120                 125
406 Arg Leu Leu Lys Gln Lys Gln Thr Gly Glu Met Glu Ser Gln Gly Cys
407     130                 135                 140
410 Lys Tyr Val Val Trp Met Ser Phe Ser Gly Leu Gly Asn Arg Ile Ile
411 145                 150                 155                 160
414 Ser Ile Ala Ser Val Phe Leu Tyr Ala Met Leu Thr Asp Arg Val Leu
415             165                 170                 175
418 Leu Val Glu Gly Gly Glu Gln Phe Ala Asp Leu Phe Cys Glu Pro Phe
419             180                 185                 190
422 Leu Asp Thr Thr Trp Leu Leu Pro Lys Asp Phe Thr Leu Ala Ser Gln
423     195                 200                 205
426 Phe Ser Gly Phe Gly Gln Asn Ser Ala His Cys His Gly Asp Met Leu
427     210                 215                 220
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431 225                 230                 235                 240
434 Tyr Leu His Leu Ala His Asp Tyr Asn Glu His Asp Lys Met Phe Phe
435             245                 250                 255
438 Cys Glu Glu Asp Gln Asn Leu Leu Lys Asn Val Pro Trp Leu Ile Met
439             260                 265                 270
442 Arg Thr Asn Asn Phe Phe Ala Pro Ser Leu Phe Leu Ile Ser Ser Phe
443         275                 280                 285
446 Glu Glu Glu Leu Gly Met Met Phe Pro Glu Lys Gly Thr Val Phe His
447     290                 295                 300
450 His Leu Gly Arg Tyr Leu Phe His Pro Ser Asn Gln Val Trp Gly Leu
451 305                 310                 315                 320
454 Ile Thr Arg Tyr Tyr Gln Ala Tyr Leu Ala Lys Ala Asp Glu Arg Ile
455             325                 330                 335
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 12/10/2002
PATENT APPLICATION: US/10/037,311A   TIME: 15:43:39

Input Set : A:\MS00-001C2 XFTASE.txt
Output Set: N:\CRF4\12102002\J037311A.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:11; N Pos. 650,659,701,702
Seq#:12; N Pos. 276,361,386,409,433,481,490
Seq#:15; N Pos. 4,5,12,16,27,50,53,72,73,81,87,98,118,147,153,159,168,205
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VERIFICATION SUMMARY   DATE: 12/10/2002
PATENT APPLICATION: US/10/037,311A   TIME: 15:43:39

Input Set : A:\MS00-001C2 XFTASE.txt
Output Set: N:\CRF4\12102002\J037311A.raw

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